

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala  
 290 295 300  
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn  
 305 310 315 320  
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly  
 325 330 335  
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys  
 340 345 350  
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu  
 355 360 365  
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu  
 370 375 380  
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp  
 385 390 395 400  
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr  
 405 410 415  
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg  
 420 425 430

&lt;210&gt; 1097

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXC02665

&lt;400&gt; 1097

caaggcgacc caatggcggtt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

atcaccgacg aagccgaacc cacaatattt gaggtaccag gtg act aac cca atc 115  
 Val Thr Asn Pro Ile 5  
 1

atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163  
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly 20  
 10 15

aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211  
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys 35  
 25 30

gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259  
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala 50  
 40 45

ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307  
 Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val  
     55                    60                    65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355  
 Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu  
     70                    75                    80                    85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403  
 Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala  
                     90                    95                    100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451  
 Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu  
                     105                    110                    115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499  
 Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser  
                     120                    125                    130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547  
 Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg  
     135                    140                    145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600  
 Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
     150                    155                    160

ggc 603

&lt;210&gt; 1098

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1098

Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His  
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Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu  
                     20                    25                    30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His  
                     35                    40                    45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly  
     50                    55                    60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr  
     65                    70                    75                    80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val  
                     85                    90                    95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly  
                     100                    105                    110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala  
     115                    120                    125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly  
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 Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 145 150 155 160

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1666)  
 <223> RXC02770

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 Met Leu Val Ala Ala  
 1 5  
 tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163  
 Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His  
 10 15 20  
 caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211  
 Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr  
 25 30 35  
 aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259  
 Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala  
 40 45 50  
 gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307  
 Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met  
 55 60 65  
 att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355  
 Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn  
 70 75 80 85  
 cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403  
 Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly  
 90 95 100  
 cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451  
 Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln  
 105 110 115  
 atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499  
 Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu  
 120 125 130  
 cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547  
 Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu 150 155 160 165			595
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu 170 175 180			643
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro 185 190 195			691
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu 200 205 210			739
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe 215 220 225			787
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala 230 235 240 245			835
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala 250 255 260			883
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu 265 270 275			931
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile 280 285 290			979
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc 1027 Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala 295 300 305			
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt 1075 Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val 310 315 320 325			
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat 1123 Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp 330 335 340			
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg 1171 Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val 345 350 355			
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat 1219 His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

360 365 370  
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga  
 1267  
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly  
 375 380 385  
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt  
 1315  
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys  
 390 395 400 405  
 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt  
 1363  
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser  
 410 415 420  
 ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag  
 1411  
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln  
 425 430 435  
 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat  
 1459  
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His  
 440 445 450  
 cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg  
 1507  
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr  
 455 460 465  
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta  
 1555  
 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu  
 470 475 480 485  
 gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt  
 1603  
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val  
 490 495 500  
 gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg  
 1651  
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp  
 505 510 515  
 tcc aga agt gag gaa taagtagtga gcgaacaagc tct  
 1689  
 Ser Arg Ser Glu Glu  
 520

&lt;210&gt; 1100

&lt;211&gt; 522

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1100

Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro  
 1 5 10 15

Glu	Pro	Thr	Ser 20	His	Gln	Thr	Ser	Leu 25	Phe	Gly	Tyr	Ala	Val 30	Asn	Ser
Ser	Leu	Ala 35	Thr	Thr	Asn	Ala	Ala	Ser	Leu	Leu	Gly	Val 45	Ala	Asn	Asp
Ala	Gly 50	Leu	Leu	Ala	Ala	Arg 55	Val	Tyr	Pro	Gly	Val 60	Tyr	Val	Gln	Gly
Pro 65	Ser	Gly	Gln	Met	Ile 70	Pro	Asn	Thr	Asp	Leu 75	Ala	Ser	Thr	Gln	Val 80
Leu	Pro	Gly	Ile	Asn 85	Arg	Gln	Val	Ile	Tyr 90	Thr	Ile	Asn	Glu	Asp 95	Ala
Thr	Tyr	Ser	Asp 100	Gly	Gln	Pro	Val	Val 105	Cys	Asp	Asp	Phe	Leu 110	Leu	Ser
Ala	Thr	Ala 115	Gly	Gln	Met	Pro	Glu 120	Leu	Phe	Gln	Ser	His 125	Val	Pro	Leu
Thr	Ser 130	Gln	Ile	Glu	Arg	Val 135	Asp	Cys	Val	Ser	Gly 140	Ser	Lys	Val	Ala
Thr 145	Val	Val	Phe	Lys	Glu 150	Asp	Leu	Gly	Glu	Arg 155	Trp	Arg	Tyr	Leu	Phe 160
Glu	Gln	Gly	Asp	Leu 165	Leu	Pro	Ala	His 170	Ala	Val	Ala	Ser	Lys	Ala 175	Gly
Met	Thr	Leu	Glu 180	Glu	Leu	Asn	Gln 185	Ala	Leu	Lys	Asp	Lys	Asp 190	Pro	Glu
Ala	Leu	Thr 195	Glu	Pro	Ala	Arg	Val 200	Trp	Ser	Glu	Gly	Phe 205	Gln	Leu	Ser
Gln	Phe 210	Asp	Pro	Glu	Leu	Gln 215	Thr	Ala	Phe	Gly	Pro 220	Tyr	Lys	Val	Asp
Ser 225	Val	Gly	Glu	Phe	Gly 230	Glu	Val	Lys	Leu	Val 235	Arg	Asn	Glu	Phe	Tyr 240
Ser	Gly	Asp	Gln	Ala 245	Val	Glu	Ala	Glu	Ile 250	Thr	Met	Trp	Pro	Lys 255	Gly
Ser	Asp	Leu	Ser 260	Ala	Ile	Ala	Asp 265	Asn	Gly	Asn	Leu	Gln	Ile 270	Ala	His
Val	Val	Ala 275	Trp	Glu	Ser	Glu	Pro 280	Trp	Val	Asn	Arg	Asp 285	Asp	Pro	Leu
Asn	Pro 290	Tyr	Asp	Ile	Lys	Glu 295	Glu	Val	Gly	Val	Leu 300	Thr	Glu	Gln	Leu
Thr 305	Leu	Ala	Ser	Ala	Gly 310	Val	Phe	Tyr	Ala	Ala 315	Glu	Ala	Arg	Gln	Ala 320
Phe	Ala	Ala	Cys	Val 325	Asp	Gln	Glu	Ala	Val 330	Ala	Ala	Ala	Ser	Ser 335	Ser

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His  
 340 345 350  
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met  
 355 360 365  
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg  
 370 375 380  
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala  
 385 390 395 400  
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser  
 405 410 415  
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu  
 420 425 430  
 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg  
 435 440 445  
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr  
 450 455 460  
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val  
 465 470 475 480  
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg  
 485 490 495  
 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp  
 500 505 510  
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu  
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<210> 1101  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(385)  
 <223> RXC02238

<400> 1101  
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 Val Thr Asn Val Ser  
 1 5  
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20  
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
           40                          45                          50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
           55                          60                          65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
       70                          75                          80                          85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           90                          95

cac 408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
       1                          5                          10                          15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
           20                          25                          30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
           35                          40                          45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
       50                          55                          60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
       65                          70                          75                          80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           85                          90                          95

<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

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 Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly  
       1                          5                          10                          15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96



Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu	
			20					25					30			
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln	
		35					40					45				
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly	
		50					55				60					
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	
		65			70					75					80	
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His	
				85					90					95		
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala	
			100					105					110			
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp	
		115					120					125				
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp	
		130				135					140					
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly	
					150					155					160	
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala	
				165					170					175		
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn	
			180					185					190			
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro	
		195					200					205				
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr	
		210				215					220					
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile	
					230					235					240	
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggt	gca	ggt	aaa	768
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys	
				245					250					255		
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggt	gtg	gaa	cgc	acc	gac	ggc	gaa	816
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu	

260						265						270						
ggc ggc atc gtc acc gga tac	ggc ctc aaa atc ggc tac ttc gcc cag	864																
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr Phe Ala Gln																	
275	280	285																
gaa cac gac acc atc gac ccc gac	aaa tcc gtc tgg caa aac acc atc	912																
Glu His Asp Thr Ile Asp Pro Asp	Lys Ser Val Trp Gln Asn Thr Ile																	
290	295	300																
gaa gcc tgc gcc gac gcc gac	caa caa agc ctc cgc agc ctc ctc gga	960																
Glu Ala Cys Ala Asp Ala Asp	Gln Gln Ser Leu Arg Ser Leu Leu Gly																	
305	310	315	320															
tcc ttc atg ttc tcc ggc gaa caa ctc	gac caa cca gca gga aca ctc																	
1008																		
Ser Phe Met Phe Ser Gly Glu Gln	Leu Asp Gln Pro Ala Gly Thr Leu																	
325	330	335																
tcc ggc ggt gaa aaa acc cgc ctc	gca ctg gcc acc ctc gtg tcc tcc																	
1056																		
Ser Gly Gly Glu Lys Thr Arg Leu	Ala Leu Ala Thr Leu Val Ser Ser																	
340	345	350																
cgc gca aac gtc ctg ctt ctc gac	gag ccc acc aac aac ctt gac ccg																	
1104																		
Arg Ala Asn Val Leu Leu Leu Asp	Glu Pro Thr Asn Asn Leu Asp Pro																	
355	360	365																
atc tcc cgc gaa cag gtc ctc gac	gca ctg cgc acc tac acc ggc gca																	
1152																		
Ile Ser Arg Glu Gln Val Leu Asp	Ala Leu Arg Thr Tyr Thr Gly Ala																	
370	375	380																
gtc gtc ctg gtt acc cac gac ccg	ggt gca gtc aag gcc ctt gag cca																	
1200																		
Val Val Leu Val Thr His Asp Pro	Gly Ala Val Lys Ala Leu Glu Pro																	
385	390	395	400															
gaa cgc gtc atc gtg ctt cct gat	ggc acc gag gat ctt tgg aat gat																	
1248																		
Glu Arg Val Ile Val Leu Pro Asp	Gly Thr Glu Asp Leu Trp Asn Asp																	
405	410	415																
cag tac atg gaa atc gtg gaa ttg	gcg taggttctaa ggctgtttat																	
1295																		
Gln Tyr Met Glu Ile Val Glu Leu	Ala																	
420	425																	

gct  
1298

<210> 1104  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1104  
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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu  
 20 25 30  
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln  
 35 40 45  
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly  
 50 55 60  
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His  
 65 70 75 80  
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His  
 85 90 95  
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala  
 100 105 110  
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp  
 115 120 125  
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp  
 130 135 140  
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly  
 145 150 155 160  
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala  
 165 170 175  
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn  
 180 185 190  
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro  
 195 200 205  
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr  
 210 215 220  
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile  
 225 230 235 240  
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys  
 245 250 255  
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu  
 260 265 270  
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln  
 275 280 285  
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile  
 290 295 300  
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly  
 305 310 315 320  
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu  
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser  
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro  
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala  
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro  
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp  
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala  
 420 425

<210> 1105  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(613)  
 <223> RXN03171

<400> 1105  
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cggtcttctt ctgggaggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
 170

&lt;210&gt; 1106

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
 1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
 165 170

&lt;210&gt; 1107

<211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> FRXA02857

<400> 1107

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cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
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<210> 1108  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1108

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Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
      20           25           30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
      35           40           45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
      50           55           60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
      65           70           75           80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
      85           90           95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
      100          105          110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
      115          120          125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
      130          135          140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
      145          150          155          160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
      165          170
  
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<210> 1109  
 <211> 424  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN00450

<400> 1109

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
              Val Gly Val Leu Pro
              1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
      10           15           20
  
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gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
25 30 35  
  
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
40 45 50  
  
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
55 60 65  
  
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
70 75 80 85  
  
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
90 95 100  
  
ggt gct cga atc gga cgc atc 424  
Gly Ala Arg Ile Gly Arg Ile  
105

&lt;210&gt; 1110

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1110

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
1 5 10 15  
  
Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
20 25 30  
  
Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
35 40 45  
  
Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
50 55 60  
  
Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
65 70 75 80  
  
Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
85 90 95  
  
Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile  
100 105

&lt;210&gt; 1111

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (418)



&lt;223&gt; FRXA00450

&lt;400&gt; 1111

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gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro 5  
 1

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu 20  
 10 15

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val 35  
 25 30

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg 50  
 40 45

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg 65  
 55 60

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr 85  
 70 75 80

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val 100  
 90 95

ggt gct cga atc gga 418  
 Gly Ala Arg Ile Gly 105

&lt;210&gt; 1112

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1112

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly  
 100 105

<210> 1113  
 <211> 615  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(592)  
 <223> RXA00465

<400> 1113  
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 Met Thr Glu Asp Asp  
 1 5  
 tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163  
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys  
 10 15 20  
 cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211  
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Val Asp Pro Phe Gly Ala  
 25 30 35  
 gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259  
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys  
 40 45 50  
 cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307  
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala  
 55 60 65  
 tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355  
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala  
 70 75 80 85  
 atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403  
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys  
 90 95 100  
 gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451  
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala  
 105 110 115  
 gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499  
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn  
 120 125 130  
 ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547  
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu  
 135 140 145  
 ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592  
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu  
 150 155 160

tagcgctggg catgtgactt taa

615

&lt;210&gt; 1114

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1114

Met	Thr	Glu	Asp	Asp	Leu	Asp	Leu	Leu	His	Arg	Thr	Val	Glu	Leu	Ala
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Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
			20					25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
		35					40					45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
	50					55					60				

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
65					70					75					80

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
				85					90					95	

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
			100					105					110		

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
		115					120					125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
	130					135					140				

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
145					150					155					160

Asn Lys Ala Leu

&lt;210&gt; 1115

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; RXA00717

&lt;400&gt; 1115

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				Val	Thr	Pro	Pro	Ala	
				1				5	

cgc	cga	gat	ggc	aca	ccg	gac	aag	aag	cag	agc	aat	cgc	tct	ggc	gga	163
Arg	Arg	Asp	Gly	Thr	Pro	Asp	Lys	Lys	Gln	Ser	Asn	Arg	Ser	Gly	Gly	
				10					15					20		
tac	cgg	tct	tca	gtt	cgt	ggc	tac	aag	cca	gga	tca	tcc	cgc	cca	aac	211
Tyr	Arg	Ser	Ser	Val	Arg	Gly	Tyr	Lys	Pro	Gly	Ser	Ser	Arg	Pro	Asn	
			25					30					35			
aca	cgc	cag	cag	cct	cag	aag	aag	gat	gag	att	ctt	ctc	tcc	aac	gct	259
Thr	Arg	Gln	Gln	Pro	Gln	Lys	Lys	Asp	Glu	Ile	Leu	Leu	Ser	Asn	Ala	
		40				45					50					
aag	cct	gcc	aag	aag	caa	aac	gta	aaa	tcc	gac	gac	gat	tgg	tcg	atg	307
Lys	Pro	Ala	Lys	Lys	Gln	Asn	Val	Lys	Ser	Asp	Asp	Asp	Trp	Ser	Met	
	55					60					65					
ggt	ttc	tta	aac	cgc	aat	gac	tct	gac	gga	gtt	cgc	ctg	cag	aag	gtg	355
Gly	Phe	Leu	Asn	Arg	Asn	Asp	Ser	Asp	Gly	Val	Arg	Leu	Gln	Lys	Val	
	70				75				80						85	
ctt	gcc	caa	gca	ggt	gtg	gca	tca	cgt	cga	cac	gca	gaa	atc	ctg	att	403
Leu	Ala	Gln	Ala	Gly	Val	Ala	Ser	Arg	Arg	His	Ala	Glu	Ile	Leu	Ile	
				90					95					100		
gat	cag	ggc	cgt	gtg	gag	gtc	aac	gat	cgt	atc	gtg	acc	acc	cag	ggc	451
Asp	Gln	Gly	Arg	Val	Glu	Val	Asn	Asp	Arg	Ile	Val	Thr	Thr	Gln	Gly	
			105					110					115			
gtg	cgc	gtg	gat	cca	aac	aac	gat	gtc	atc	cgt	gtt	gac	ggc	gtc	cgc	499
Val	Arg	Val	Asp	Pro	Asn	Asn	Asp	Val	Ile	Arg	Val	Asp	Gly	Val	Arg	
		120					125					130				
atc	cac	atc	aac	gag	gac	ctc	gag	tac	ttc	gtg	ctc	aac	aag	cct	cgt	547
Ile	His	Ile	Asn	Glu	Asp	Leu	Glu	Tyr	Phe	Val	Leu	Asn	Lys	Pro	Arg	
	135					140					145					
ggc	atg	cac	tcc	acc	atg	agc	gat	gaa	ctt	ggt	cgc	cca	tgc	gtg	ggt	595
Gly	Met	His	Ser	Thr	Met	Ser	Asp	Glu	Leu	Gly	Arg	Pro	Cys	Val	Gly	
	150				155				160						165	
gat	ctg	gtc	agt	gag	aag	act	gca	tct	gga	cag	cgt	ctg	ttc	cac	gtc	643
Asp	Leu	Val	Ser	Glu	Lys	Thr	Ala	Ser	Gly	Gln	Arg	Leu	Phe	His	Val	
				170					175					180		
ggt	cgc	ctc	gac	gcg	gac	acc	gaa	ggt	ttg	ctg	ctg	ctc	acc	aac	gat	691
Gly	Arg	Leu	Asp	Ala	Asp	Thr	Glu	Gly	Leu	Leu	Leu	Leu	Thr	Asn	Asp	
			185				190						195			
ggt	gag	ttg	gct	aac	cgc	ctc	atg	cac	cct	aag	tac	gaa	gtg	tcc	aag	739
Gly	Glu	Leu	Ala	Asn	Arg	Leu	Met	His	Pro	Lys	Tyr	Glu	Val	Ser	Lys	
		200					205					210				
act	tac	ctt	gct	acc	gtt	cgc	ggt	gaa	gca	acc	aat	aag	cta	gtc	agc	787
Thr	Tyr	Leu	Ala	Thr	Val	Arg	Gly	Glu	Ala	Thr	Asn	Lys	Leu	Val	Ser	
	215					220					225					
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Ala	Leu	Arg	Asp	Gly	Val	Glu	Leu	Glu	Asp	Gly	Pro	Ala	Lys	Ala	Asp	
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Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
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 gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
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 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
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 cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct  
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 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val  
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 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile  
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 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg  
 115 120 125  
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val  
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 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly  
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln  
 165 170 175  
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu  
 180 185 190  
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys  
 195 200 205  
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr  
 210 215 220  
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly  
 225 230 235 240  
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys  
 245 250 255  
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg  
 260 265 270  
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr  
 275 280 285  
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg  
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 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
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&lt;210&gt; 1117

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXA01894

&lt;400&gt; 1117

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 Met Pro Lys Pro Lys  
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aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163  
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly  
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 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp  
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tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259  
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

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Ile	Gly	Gly	Gln	Ala	Ile	Ile	Trp	Leu	Ser	Trp	Pro	Phe	Gly	Thr	Met	
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Gly	Ile	Leu	Ala	Ser	Phe	Val	Ala	Thr	Val	Leu	Val	Leu	Met	Tyr	Phe	
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Arg	Ile	Phe	Tyr	Asn	Gly	Thr	Glu	Lys	Glu	Ala	Arg	Asn	Tyr	Leu	Arg	
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Asp	Thr	Ser	Val	Gly	Ile	Phe	Val	Leu	Thr	Trp	Ile	Pro	Leu	Phe	Gly	
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Ser	Phe	Ala	Ala	Met	Leu	Ser	Leu	Met	Gln	Asn	Asn	Ser	Ile	Pro	Gly	
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aca	tat	ttc	att	ttg	acg	ttc	atg	ctg	tgt	gtg	atc	gca	tcg	gat	gtg	595
Thr	Tyr	Phe	Ile	Leu	Thr	Phe	Met	Leu	Cys	Val	Ile	Ala	Ser	Asp	Val	
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Gly	Gly	Tyr	Ile	Ala	Gly	Val	Phe	Phe	Gly	Ser	His	Pro	Met	Ala	Pro	
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Leu	Val	Ser	Pro	Lys	Lys	Ser	Trp	Glu	Gly	Phe	Ala	Gly	Ser	Ile	Val	
			185					190					195			
tta	gga	tcg	gtc	act	ggt	gca	ctc	agt	gtt	cac	ttc	ctg	ctc	gat	cac	739
Leu	Gly	Ser	Val	Thr	Gly	Ala	Leu	Ser	Val	His	Phe	Leu	Leu	Asp	His	
		200					205					210				
cac	tgg	tgg	atg	ggt	gtg	atc	ttg	ggt	tgt	gcc	cta	gtt	gtg	tgc	gcc	787
His	Trp	Trp	Met	Gly	Val	Ile	Leu	Gly	Cys	Ala	Leu	Val	Val	Cys	Ala	
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Lys	Asp	Met	Ser	Asn	Leu	Leu	Pro	Gly	His	Gly	Gly	Leu	Met	Asp	Arg	
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Leu	Asp	Gly	Met	Leu	Pro	Ala	Ala	Met	Val	Thr	Trp	Leu	Ile	Leu	Ser	
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gtg	atc	agc	agc	tcg	tat	ccg	tcg	taaagcttgg gccagcttta agt								978
Val	Ile	Ser	Ser	Ser	Tyr	Pro	Ser									
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&lt;210&gt; 1118

&lt;211&gt; 285

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1118

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Ser	Pro	Trp	Gly	Trp	Tyr	Ile	Leu	Val	Ala	Gly	Phe	Met	Ala	Ala	Ala
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Thr	Trp	Glu	Val	Gly	Ser	Arg	Leu	Lys	Glu	Gly	Gly	Tyr	His	Leu	Pro
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Leu	Pro	Ile	Met	Ile	Ile	Gly	Gly	Gln	Ala	Ile	Ile	Trp	Leu	Ser	Trp
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Pro	Phe	Gly	Thr	Met	Gly	Ile	Leu	Ala	Ser	Phe	Val	Ala	Thr	Val	Leu
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Val	Leu	Met	Tyr	Phe	Arg	Ile	Phe	Tyr	Asn	Gly	Thr	Glu	Lys	Glu	Ala
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Arg	Asn	Tyr	Leu	Arg	Asp	Thr	Ser	Val	Gly	Ile	Phe	Val	Leu	Thr	Trp
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Ile	Pro	Leu	Phe	Gly	Ser	Phe	Ala	Ala	Met	Leu	Ser	Leu	Met	Gln	Asn
	130					135					140				

Asn	Ser	Ile	Pro	Gly	Thr	Tyr	Phe	Ile	Leu	Thr	Phe	Met	Leu	Cys	Val
145					150					155					160

Ile	Ala	Ser	Asp	Val	Gly	Gly	Tyr	Ile	Ala	Gly	Val	Phe	Phe	Gly	Ser
				165					170					175	

His	Pro	Met	Ala	Pro	Leu	Val	Ser	Pro	Lys	Lys	Ser	Trp	Glu	Gly	Phe
			180					185					190		

Ala	Gly	Ser	Ile	Val	Leu	Gly	Ser	Val	Thr	Gly	Ala	Leu	Ser	Val	His
		195					200					205			

Phe	Leu	Leu	Asp	His	His	Trp	Trp	Met	Gly	Val	Ile	Leu	Gly	Cys	Ala
	210					215					220				

Leu	Val	Val	Cys	Ala	Thr	Leu	Gly	Asp	Leu	Val	Glu	Ser	Gln	Phe	Lys
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Arg	Asp	Leu	Gly	Ile	Lys	Asp	Met	Ser	Asn	Leu	Leu	Pro	Gly	His	Gly
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Gly	Leu	Met	Asp	Arg	Leu	Asp	Gly	Met	Leu	Pro	Ala	Ala	Met	Val	Thr
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Trp	Leu	Ile	Leu	Ser	Val	Ile	Ser	Ser	Ser	Tyr	Pro	Ser
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ctg	ctg	cgt	gat	gct	gct	gaa	aaa	gct	gcg	gaa	cag	ggg	gct	cgg	gtg	163
Leu	Leu	Arg	Asp	Ala	Ala	Glu	Lys	Ala	Ala	Glu	Gln	Gly	Ala	Arg	Val	
				10				15						20		
ttg	gtg	ttt	ccg	gag	gcg	act	tcg	caa	agc	ttt	ggg	acg	gga	agg	ctt	211
Leu	Val	Phe	Pro	Glu	Ala	Thr	Ser	Gln	Ser	Phe	Gly	Thr	Gly	Arg	Leu	
			25					30					35			
gat	act	cag	gcg	gag	gag	ctc	gat	ggc	gaa	ttc	tcc	acc	gcg	gta	cga	259
Asp	Thr	Gln	Ala	Glu	Glu	Leu	Asp	Gly	Glu	Phe	Ser	Thr	Ala	Val	Arg	
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aaa	tta	gcc	gat	gag	ctg	gac	gtt	gtc	atc	gtt	gcg	ggc	atg	ttc	acc	307
Lys	Leu	Ala	Asp	Glu	Leu	Asp	Val	Val	Ile	Val	Ala	Gly	Met	Phe	Thr	
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cct	gct	gac	acc	gtg	cag	cgc	ggg	gaa	aaa	acg	atc	tcg	cgc	gtc	aac	355
Pro	Ala	Asp	Thr	Val	Gln	Arg	Gly	Glu	Lys	Thr	Ile	Ser	Arg	Val	Asn	
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Asn	Thr	Val	Leu	Ile	Ser	Gly	Ala	Gly	Leu	His	Gln	Gly	Tyr	Asn	Lys	
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Ile	His	Thr	Tyr	Asp	Ala	Phe	Gly	Tyr	Arg	Glu	Ser	Asp	Thr	Val	Lys	
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Pro	Gly	Asp	Glu	Leu	Val	Val	Phe	Glu	Val	Asp	Asp	Ile	Lys	Phe	Gly	
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Val	Ala	Thr	Cys	Tyr	Asp	Ile	Arg	Phe	Pro	Glu	Gln	Phe	Lys	Asp	Leu	
	135					140					145					
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Glu	Glu	Leu	Arg	Asp	Glu	Arg	Lys	Gly	Pro	Thr	Gly	Ile	Gly	His	Ser	
		200					205					210				
atg	gtg	aca	aac	cca	cac	ggg	gaa	gta	att	gct	agc	gcg	ggg	tat	gag	787
Met	Val	Thr	Asn	Pro	His	Gly	Glu	Val	Ile	Ala	Ser	Ala	Gly	Tyr	Glu	
	215					220					225					
cca	gaa	atg	ttg	atc	gcg	gat	att	gat	gtc	agc	ggg	ttg	gcc	aaa	att	835
Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser	Gly	Leu	Ala	Lys	Ile	
230					235				240						245	
cgg	gag	gca	ttg	cct	ggt	ctt	taaccactgt ctaaggaatc act									879
Arg	Glu	Ala	Leu	Pro	Val	Leu										
				250												

&lt;210&gt; 1120

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1120

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Gly	Thr	Gly	Arg	Leu	Asp	Thr	Gln	Ala	Glu	Glu	Leu	Asp	Gly	Glu	Phe	
		35					40					45				
Ser	Thr	Ala	Val	Arg	Lys	Leu	Ala	Asp	Glu	Leu	Asp	Val	Val	Ile	Val	
	50					55					60					
Ala	Gly	Met	Phe	Thr	Pro	Ala	Asp	Thr	Val	Gln	Arg	Gly	Glu	Lys	Thr	
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Ile	Ser	Arg	Val	Asn	Asn	Thr	Val	Leu	Ile	Ser	Gly	Ala	Gly	Leu	His	
				85					90					95		
Gln	Gly	Tyr	Asn	Lys	Ile	His	Thr	Tyr	Asp	Ala	Phe	Gly	Tyr	Arg	Glu	
			100					105					110			
Ser	Asp	Thr	Val	Lys	Pro	Gly	Asp	Glu	Leu	Val	Val	Phe	Glu	Val	Asp	
		115					120					125				
Asp	Ile	Lys	Phe	Gly	Val	Ala	Thr	Cys	Tyr	Asp	Ile	Arg	Phe	Pro	Glu	
	130					135					140					
Gln	Phe	Lys	Asp	Leu	Ala	Arg	Asn	Gly	Ala	Gln	Ile	Ile	Val	Val	Pro	
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Thr	Ser	Trp	Gln	Asp	Gly	Pro	Gly	Lys	Leu	Glu	Gln	Trp	Glu	Val	Leu	
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Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr  
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala  
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 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
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 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
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 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val  
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 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala  
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Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
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Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
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Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
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Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
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Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
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Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
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gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
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Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
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Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
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Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
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ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
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 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
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ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
                   375                                  380                                  385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390                                  395                                  400                                  405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
                                   410                                  415                                  420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
                   425                                  430                                  435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
                   440                                  445                                  450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
                   455                                  460                                  465

gcc gcc ggc gaa agc gtg gaa  
 1528  
 Ala Ala Gly Glu Ser Val Glu  
 470                                  475

<210> 1122

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
   1                                  5                                  10                                  15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
                   20                                  25                                  30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
                   35                                  40                                  45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370		375		380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met				
385		390		400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr				
	405		410	415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn				
	420		425	430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg				
	435		440	445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser				
450		455		460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu				
465	470		475	

&lt;210&gt; 1123

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(1528)

&lt;223&gt; FRXA01209

&lt;400&gt; 1123

cagattgcag cacagaaggc atcggcgcca ggcagctttg cggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg	atg tgc gag agg cct	115
	Met Cys Glu Arg Pro	
	1 5	

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt	163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val	
10 15 20	

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att	211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile	
25 30 35	

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag	
1027 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
295 300 305	
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc	
1075 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	
1123	



Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528

Ala Ala Gly Glu Ser Val Glu  
 470 475

<210> 1124

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
 1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45  
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355	360	365
Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn		
370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410
		415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425
		430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
	435	440
		445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
450	455	460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475

&lt;210&gt; 1125

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(772)

&lt;223&gt; RXN01617

&lt;400&gt; 1125

tcagaagcta ccggcggcgc cggcatccag gttgatttga agaccttcca gcattttaaga 60

tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca	115
Leu Ile Leu Lys Thr	
1 5	

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat	163
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn	
10 15 20	

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc	211
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile	
25 30 35	

ggc atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg	259
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu	
40 45 50	

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc	307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys	
55 60 65	

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc	355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg	
70 75 80 85	

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403  
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu  
                     90                                    95                                    100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451  
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu  
                     105                                    110                                    115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499  
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val  
                     120                                    125                                    130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547  
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu  
                     135                                    140                                    145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595  
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp  
 150                                    155                                    160                                    165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643  
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala  
                     170                                    175                                    180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691  
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys  
                     185                                    190                                    195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739  
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro  
                     200                                    205                                    210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792  
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                     215                                    220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala  
     1                    5                                    10                                    15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu  
                     20                                    25                                    30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                     35                                    40                                    45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
                     50                                    55                                    60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
                     65                                    70                                    75                                    80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85					90					95					
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu
			100					105					110		
Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly
		115					120					125			
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn
	130					135					140				
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu
145					150					155					160
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala
				165					170					175	
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala
			180					185						190	
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val
		195					200					205			
Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys
	210					215					220				

&lt;210&gt; 1127

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(615)

&lt;223&gt; FRXA01617

&lt;400&gt; 1127

gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg	48
Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val	
1				5				10						15		
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20					25					30			
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	
		35					40					45				
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
	50					55					60					
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65					70					75					80	

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288  
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                     85                    90                    95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336  
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
                     100                    105                    110

gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384  
 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
                     115                    120                    125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432  
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
                     130                    135                    140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480  
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
 145                    150                    155                    160

acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528  
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
                     165                    170                    175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576  
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
                     180                    185                    190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt 625  
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                     195                    200                    205

aaacaagctc cct 638

&lt;210&gt; 1128

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1128

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
 1                    5                    10                    15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
                     20                    25                    30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
                     35                    40                    45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
                     50                    55                    60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
 65                    70                    75                    80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                     85                    90                    95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
                     100                    105                    110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
 195 200 205

<210> 1129  
 <211> 792  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(769)  
 <223> RXC01600

<400> 1129  
 tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tcg aag atg 115  
 Met Val Ser Lys Met  
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163  
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu  
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211  
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro  
 25 30 35

ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259  
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val  
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gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307  
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr  
 55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355  
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu  
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403  
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met  
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451  
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu  
 105 110 115  
 att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499  
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala  
 120 125 130  
 cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547  
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu  
 135 140 145  
 gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595  
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met  
 150 155 160 165  
 gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643  
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met  
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 gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691  
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr  
 185 190 195  
 gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739  
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala  
 200 205 210  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu  
 35 40 45  
 His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala  
 50 55 60  
 Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu  
 65 70 75 80  
 Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala  
 85 90 95  
 Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser  
 100 105 110



Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val  
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val  
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His  
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala  
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser  
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala  
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu  
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 <213> Corynebacterium glutamicum

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 <223> RXC01622

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 Met Ser Asp Phe Tyr  
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163  
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly  
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211  
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg  
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259  
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val  
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307  
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu  
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355  
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro  
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val  
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 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val  
 105 110 115  
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499  
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu  
 120 125 130  
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547  
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu  
 135 140 145  
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595  
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro  
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 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met  
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 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691  
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp  
 185 190 195  
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 Pro Ser Asp Asn  
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&lt;210&gt; 1132

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn  
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 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser  
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 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala  
 35 40 45  
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala  
 50 55 60  
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu  
 65 70 75 80  
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val  
 85 90 95  
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu  
 100 105 110  
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val  
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp  
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val  
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile  
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Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser  
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Thr Phe Pro Ser Asp Pro Ser Asp Asn  
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 Val Ser Lys Ile Ser 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
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Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
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Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
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Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
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Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
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Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
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cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	
1027	
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
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1075	
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
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agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	
1123	
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	

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 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
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 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
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gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
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 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
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gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
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 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485

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 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
 1747  
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
 535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
 1795  
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 Val Ala Tyr

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 <211> 568  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1134  
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 Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
 35 40 45  
 Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
 50 55 60  
 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
 65 70 75 80  
 Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
 85 90 95  
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110  
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
 115 120 125  
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
 130 135 140  
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
 145 150 155 160  
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
 165 170 175  
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190  
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro





gat

555

&lt;210&gt; 1136

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly  
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Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser  
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Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly  
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg  
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys  
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser  
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser  
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu  
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 130 135 140

&lt;210&gt; 1137

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(898)

&lt;223&gt; RXC02207

&lt;400&gt; 1137

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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115  
 Met Arg Arg Arg Ser  
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163  
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala  
 10 15 20

ctt	ctt	tta	agt	gca	tgt	acg	caa	ggg	gta	acg	gac	tcc	ccg	gat	atg	211
Leu	Leu	Leu	Ser	Ala	Cys	Thr	Gln	Gly	Val	Thr	Asp	Ser	Pro	Asp	Met	
			25					30					35			
ggc	aag	gca	act	ccc	gct	gtc	tcc	ccc	gca	gca	agc	aac	ccg	gat	ggc	259
Gly	Lys	Ala	Thr	Pro	Ala	Val	Ser	Pro	Ala	Ala	Ser	Asn	Pro	Asp	Gly	
		40					45					50				
caa	gta	att	gag	ttc	ggc	aac	atc	act	gac	atg	gaa	gtc	act	gat	ggc	307
Gln	Val	Ile	Glu	Phe	Gly	Asn	Ile	Thr	Asp	Met	Glu	Val	Thr	Asp	Gly	
	55					60					65					
gac	atc	ctc	ggc	gta	cgc	acc	gaa	gac	gca	ctc	gct	att	ggc	aca	gtc	355
Asp	Ile	Leu	Gly	Val	Arg	Thr	Glu	Asp	Ala	Leu	Ala	Ile	Gly	Thr	Val	
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tcc	gac	ttc	gaa	gcg	ggc	agc	cag	gtg	gaa	ctg	gac	gtc	gat	aag	caa	403
Ser	Asp	Phe	Glu	Ala	Gly	Ser	Gln	Val	Glu	Leu	Asp	Val	Asp	Lys	Gln	
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tgc	ggc	gac	ctg	acc	gca	acc	ggc	ggc	act	ttc	gtg	ctc	ccc	tgc	gcc	451
Cys	Gly	Asp	Leu	Thr	Ala	Thr	Gly	Gly	Thr	Phe	Val	Leu	Pro	Cys	Ala	
			105				110						115			
gat	ggc	gtt	tat	ttg	att	gat	gcc	aag	gac	ccg	gat	ctg	gat	gag	ttg	499
Asp	Gly	Val	Tyr	Leu	Ile	Asp	Ala	Lys	Asp	Pro	Asp	Leu	Asp	Glu	Leu	
		120					125					130				
cgt	gca	act	gac	aag	cca	gtc	acg	gtg	gca	gcc	ttg	acc	agc	gat	gat	547
Arg	Ala	Thr	Asp	Lys	Pro	Val	Thr	Val	Ala	Ala	Leu	Thr	Ser	Asp	Asp	
	135					140					145					
cag	ctt	ctg	gtg	ggc	aat	ggc	gaa	gat	gaa	gaa	ctc	acc	atc	tac	cgc	595
Gln	Leu	Leu	Val	Gly	Asn	Gly	Glu	Asp	Glu	Glu	Leu	Thr	Ile	Tyr	Arg	
150					155					160					165	
gag	ggc	gaa	gag	cca	gaa	acc	ttc	acc	gtc	gcg	ggc	ccc	aac	acc	cag	643
Glu	Gly	Glu	Glu	Pro	Glu	Thr	Phe	Thr	Val	Ala	Gly	Pro	Asn	Thr	Gln	
				170					175					180		
ctc	atc	gcc	gtt	cct	gtc	att	gat	cgc	cac	gac	gcc	gtt	gtg	cgc	acc	691
Leu	Ile	Ala	Val	Pro	Val	Ile	Asp	Arg	His	Asp	Ala	Val	Val	Arg	Thr	
			185					190					195			
tgg	aac	gaa	aac	acc	acg	att	caa	gat	gtg	gac	tac	ccc	aac	gac	cgt	739
Trp	Asn	Glu	Asn	Thr	Thr	Ile	Gln	Asp	Val	Asp	Tyr	Pro	Asn	Asp	Arg	
		200					205					210				
gaa	ggc	gcg	acc	ctt	cgc	gtg	gga	ctc	ggc	gtt	ggc	caa	atg	gct	ggc	787
Glu	Gly	Ala	Thr	Leu	Arg	Val	Gly	Leu	Gly	Val	Gly	Gln	Met	Ala	Gly	
	215					220					225					
ggc	gaa	gac	ggc	ctg	ctg	gtg	gtc	tct	gat	gaa	atg	ggc	ggc	caa	att	835
Gly	Glu	Asp	Gly	Leu	Leu	Val	Val	Ser	Asp	Glu	Met	Gly	Gly	Gln	Ile	
230					235					240					245	
gcc	atc	tac	aac	gct	gat	gat	gtc	atc	cga	ctt	caa	aac	gac	cgc	ccc	883
Ala	Ile	Tyr	Asn	Ala	Asp	Asp	Val	Ile	Arg	Leu	Gln	Asn	Asp	Arg	Pro	
			250						255					260		

cac cga cga gga acc  
His Arg Arg Gly Thr  
265

898

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Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala  
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Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp  
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Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val  
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Gln Asn Asp Arg Pro His Arg Arg Gly Thr  
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&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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Gly	Ser	His	Gly	Ser	Glu	Asp	Ser	Ser	Arg	Pro	Arg	Thr	Leu	Thr	Pro
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 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala  
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 aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259  
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 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile  
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 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu  
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 Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr  
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 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly  
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 490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg  
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 His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu  
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 Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala  
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 1747  
 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn  
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 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys  
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 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln  
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 Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala  
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gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct  
 2227  
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala  
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 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly  
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 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
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Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
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Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
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Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Thr	Glu	Glu	Ser	Leu	Lys	Arg	Val	Val	Ala	Gln	Gln	Glu	Leu	Ala	Ala		
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Glu	Ile	Leu	Arg	Leu	Ala	Arg	Ala	Met	Arg	Arg	Asp	Asn	Phe	Ser	Thr		
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Ala	Gly	Thr	Asn	Val	Thr	Glu	Asp	Lys	Leu	Ser	Glu	Thr	Ile	Ile	Glu		
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Leu	Val	Ala	Ala	Met	Pro	Val	Tyr	Arg	Ala	Asp	Tyr	Ile	Ser	Leu	Ser		
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Arg	Arg	Asp	Ala	Leu	Asp	Leu	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Asn	Gly		
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Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
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 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
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 Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
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 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
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 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
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 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
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 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
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 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
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 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
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 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
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 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp  
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 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
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 Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp  
           675                                  680                                  685  
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
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 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
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 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
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Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
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Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
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 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu  
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 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro  
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tgc tcc cac acc gac ccc gag ctc aac cgg cta acc tcc gag ggc cgc  
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 Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg  
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aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc  
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 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser  
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 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe  
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act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac  
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 Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His  
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ctg cgg cac acc ttg ggc ttc tcc caa cca aac ttg ctc aca ctc gag  
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 Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg  
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att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc  
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 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly  
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Asn 225	His	Phe	Gly	Pro	Asp 230	Gly	Asn	Tyr	Asn	Gly 235	Gln	Phe	Gly	Pro	Tyr 240
Thr	Ser	Gly	Gly	Ser 245	Thr	Gly	Trp	Gly	Asp 250	Val	Val	Asn	Ile	Asn	Gly 255
His	Asp	Ser	Asp 260	Glu	Val	Arg	Asn	Tyr 265	Ile	Leu	Asp	Ala	Ala	Arg	Gln
Trp	Phe	Glu	Asp	Phe	His	Val	Asp 280	Gly	Leu	Arg	Leu	Asp 285	Ala	Val	His
Ser 290	Leu	Asp	Asp	Arg	Gly	Ala 295	Tyr	Ser	Leu	Leu	Ala 300	Gln	Leu	Thr	Met
Val 305	Ala	Glu	Asp	Val	Ser 310	Ala	Gln	Thr	Gly	Ile 315	Pro	Arg	Ser	Leu	Ile 320
Ala	Glu	Ser	Glu	Leu 325	Asn	Asp	Pro	Lys	Phe 330	Val	Thr	Ser	Arg	Glu	Ala 335
Gly	Gly	Phe	Gly	Leu 340	Asp	Ala	Gln	Trp 345	Val	Asp	Asp	Ile	His	His	Ala
Leu	His 355	Ala	Leu	Val	Ser	Gly	Glu 360	Arg	Asn	Gly	Tyr	Tyr 365	Ser	Asp	Phe
Gly 370	Ser	Val	Asp	Thr	Leu	Ala 375	Lys	Thr	Leu	Arg	Glu	Val	Phe	Glu	His
Thr 385	Gly	Asn	Tyr	Ser	Thr 390	Tyr	Arg	Gly	Arg	Asn 395	His	Gly	Arg	Pro	Val 400
His	Pro	Asp	Ile	Thr 405	Pro	Ala	Ser	Arg	Phe 410	Val	Thr	Tyr	Thr	Thr 415	Thr
His	Asp	Gln	Thr	Gly	Asn	Arg	Ala	Ile 425	Gly	Asp	Arg	Pro	Ser	Thr	Thr 430
Leu	Thr 435	Pro	Glu	Gln	Gln	Val	Leu 440	Lys	Ala	Ala	Ile	Ile 445	Tyr	Ser	Ser
Pro 450	Tyr	Thr	Pro	Met	Leu	Phe 455	Met	Gly	Glu	Glu	Phe 460	Gly	Ala	Thr	Thr
Pro 465	Phe	Ala	Phe	Phe	Cys 470	Ser	His	Thr	Asp	Pro 475	Glu	Leu	Asn	Arg	Leu 480
Thr	Ser	Glu	Gly	Arg	Lys	Arg	Glu	Phe	Ala 490	Arg	Leu	Gly	Trp	Asn	Ala 495
Asp	Asp	Ile	Pro	Ser	Pro	Glu	Leu	Glu	Ser	Thr	Phe	Thr	Ser	Ser	Lys 500
Leu	Asp 515	Trp	Glu	Phe	Thr	Ala	Glu	Gln	Arg	Arg	Ile	Asn	Asp	Ala	Tyr 525
Lys 530	Gln	Leu	Leu	His	Leu	Arg 535	His	Thr	Leu	Gly	Phe	Ser	Gln	Pro	Asn 540



Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala  
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 565 570 575  
 Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val  
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 Met Ser Ser Ile Ser 5  
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 cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163  
 Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile 20  
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 Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser 35  
 25 30  
 acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259  
 Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met 50  
 40 45  
 ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307  
 Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn 65  
 55 60  
 gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355  
 Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu 85  
 70 75 80  
 gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403  
 Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn 100  
 90 95  
 tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451  
 Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe 115  
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gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499  
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp  
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acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547  
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly  
                   135                  140                  145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595  
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg  
                   150                  155                  160                  165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643  
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val  
                   170                  175                  180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691  
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr  
                   185                  190                  195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739  
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile  
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gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787  
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg  
                   215                  220                  225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832  
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly  
                   230                  235                  240

&lt;210&gt; 1148

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1148

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Leu Leu Ala Ala Ile Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser  
                   20                  25                  30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro  
                   35                  40                  45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile  
                   50                  55                  60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn  
   65                  70                  75                  80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser  
                   85                  90                  95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile  
                   100                  105                  110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115		120		125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser				
130		135		140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly				
145		150		155
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn				
		165		170
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val				
		180		185
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn				
		195		200
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp				
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Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala				
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				235
				240
Leu Val Asp Gly				

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 Met Asn Arg Ala Arg  
 1 5  
 atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt 163  
 Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys  
 10 15 20  
 ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211  
 Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn  
 25 30 35  
 att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259  
 Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile  
 40 45 50  
 tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307  
 Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr  
 55 60 65  
 ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355

Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu  
 70 75 80 85  
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403  
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp  
 90 95 100  
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451  
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His  
 105 110 115  
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499  
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr  
 120 125 130  
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547  
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg  
 135 140 145  
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgcca 596  
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser  
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 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile  
 35 40 45  
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser  
 50 55 60  
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe  
 65 70 75 80  
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr  
 85 90 95  
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln  
 100 105 110  
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe  
 115 120 125  
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val  
 130 135 140  
 Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro  
 145 150 155 160

Thr Ser

&lt;210&gt; 1151

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (101)..(1567)

&lt;223&gt; RXS00349

&lt;400&gt; 1151

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				Met	Leu	Ser	Phe	Ala	
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acc	ctt	cgt	ggc	cgc	att	tca	aca	ggt	gac	gct	gca	aaa	gcc	gca	cct	163
Thr	Leu	Arg	Gly	Arg	Ile	Ser	Thr	Val	Asp	Ala	Ala	Lys	Ala	Ala	Pro	
			10						15					20		

ccg	cca	tcg	cca	cta	gcc	ccg	att	gat	ctc	act	gac	cat	agt	caa	gtg	211
Pro	Pro	Ser	Pro	Leu	Ala	Pro	Ile	Asp	Leu	Thr	Asp	His	Ser	Gln	Val	
			25					30					35			

gcc	ggt	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	259
Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser	
		40				45						50				

tca	ggt	acg	tca	aat	agt	gac	acc	aag	gta	caa	ggt	cga	gca	gtg	acc	307
Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr	
	55					60					65					

tct	gcg	tac	ggt	ttg	tac	tac	acg	cac	gtg	gat	atc	acg	ttg	aat	acg	355
Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	
70				75						80				85		

atc	acc	atc	ttc	acc	aac	atc	ggt	gtg	gag	agg	aag	atg	ccg	gtc	aac	403
Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	
			90						95					100		

gtg	ttt	cat	ggt	gta	ggc	aag	ttg	gac	acc	aac	ttc	tcc	aaa	ctg	tct	451
Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	
			105					110					115			

gag	ggt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggt	gcg	acc	ccg	cct	499
Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro	
		120					125					130				

gag	ggt	gcc	gag	aaa	atc	ctg	gac	gag	ttg	gag	caa	tcc	cct	gcg	tct	547
Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	
		135				140					145					

tat	ggt	ttc	cct	ggt	gcg	ttg	ctt	ggc	tgg	gca	atg	atg	ggt	ggt	gct	595
Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala	
150					155					160					165	

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Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe	
170 175 180	
att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag	691
Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys	
185 190 195	
ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg	739
Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr	
200 205 210	
ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag	787
Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu	
215 220 225	
atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca	835
Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala	
230 235 240 245	
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Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro	
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Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly	
265 270 275	
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Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His	
280 285 290	
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1027	
Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser	
295 300 305	
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1075	
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310 315 320 325	
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1123	
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330 335 340	
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Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly	
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ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt	
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Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly	
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ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att	
1267	
Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile	

375                                      380                                      385  
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg  
 1315  
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met  
 390                                      395                                      400                                      405  
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg  
 1363  
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
                                     410                                      415                                      420  
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt  
 1411  
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly  
                                     425                                      430                                      435  
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac  
 1459  
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
                                     440                                      445                                      450  
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag  
 1507  
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
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 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc  
 1555  
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe  
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 Gly Asn Lys Arg

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                                     20                                      25                                      30  
 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
                                     35                                      40                                      45  
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
                                     50                                      55                                      60  
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
   65                                      70                                      75                                      80  
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
                                     85                                      90                                      95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
 100 105 110  
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
 115 120 125  
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
 130 135 140  
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
 145 150 155 160  
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
 165 170 175  
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
 180 185 190  
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
 195 200 205  
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
 210 215 220  
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
 225 230 235 240  
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
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 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe  
 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
 355 360 365  
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415



Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
 420 425 430

Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
 435 440 445

Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys  
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Thr Asn Gln Arg Phe Gly Asn Lys Arg  
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&lt;210&gt; 1153

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(417)

&lt;223&gt; RXS03183

&lt;400&gt; 1153

gaa gcc gaa gca acc gca ggc aaa ttc gaa gta cag ccc ctc gta ggt	48
Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly	
1 5 10 15	
aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc	96
Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile	
20 25 30	
aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc	144
Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe	
35 40 45	
atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca	192
Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro	
50 55 60	
cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac	240
Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr	
65 70 75 80	
cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc	288
Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg	
85 90 95	
cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac	336
Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn	
100 105 110	
gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc	384
Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr	
115 120 125	
gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca	437
Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser	

130

135

ttc

440

&lt;210&gt; 1154

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1154

Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly  
 1 5 10 15

Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30

Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45

Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60

Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80

Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95

Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110

Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125

Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser  
 130 135

&lt;210&gt; 1155

&lt;211&gt; 1212

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1189)

&lt;223&gt; RXC00874

&lt;400&gt; 1155

agctgttccc taccattgct gaacgggagt ggattgtcac tttagcccct cacggattct 60

tctggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa 115  
 Met Ser Ile Gly Gln  
 1 5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163  
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp  
 10 15 20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn	Val	Asp	Ile	Val	Leu	Ser	Arg	Glu	Cys	Gly	Glu	Asn	Thr	Leu	Ala		
			25					30					35				
gta	gtg	cgc	atc	aac	aat	gcg	ctg	tat	cag	ttg	ttg	gtc	aat	gat	gat	259	
Val	Val	Arg	Ile	Asn	Asn	Ala	Leu	Tyr	Gln	Leu	Leu	Val	Asn	Asp	Asp		
		40					45					50					
ggc	aaa	gat	gtt	ctc	aac	gac	cac	gta	gaa	gag	gtc	ggg	gag	agt	ttc	307	
Gly	Lys	Asp	Val	Leu	Asn	Asp	His	Val	Glu	Glu	Val	Gly	Ala	Ser	Phe		
	55					60					65						
gga	gca	tgg	act	ggc	agc	tct	gct	ttt	ccc	att	ggc	cct	ttc	act	cca	355	
Gly	Ala	Trp	Thr	Gly	Ser	Ser	Ala	Phe	Pro	Ile	Gly	Pro	Phe	Thr	Pro		
70					75					80					85		
ctc	ggc	aca	gaa	caa	tcc	aat	agc	tct	ttc	atc	acc	gcc	gac	aat	aaa	403	
Leu	Gly	Thr	Glu	Gln	Ser	Asn	Ser	Ser	Phe	Ile	Thr	Ala	Asp	Asn	Lys		
				90					95					100			
gcg	atc	gtg	aaa	tac	ttc	cgc	aaa	tta	gaa	tcc	ggg	caa	aac	ccc	gat	451	
Ala	Ile	Val	Lys	Tyr	Phe	Arg	Lys	Leu	Glu	Ser	Gly	Gln	Asn	Pro	Asp		
			105					110					115				
gtg	gag	cta	att	tct	aaa	att	tcc	tcc	tgc	ccc	aac	atc	gcg	ccc	atc	499	
Val	Glu	Leu	Ile	Ser	Lys	Ile	Ser	Ser	Cys	Pro	Asn	Ile	Ala	Pro	Ile		
		120					125					130					
ctg	ggg	ttt	tcc	tcc	gct	gag	atc	tcc	ggg	gct	aac	tac	acc	ctg	gtc	547	
Leu	Gly	Phe	Ser	Ser	Ala	Glu	Ile	Ser	Gly	Ala	Asn	Tyr	Thr	Leu	Val		
	135					140					145						
atg	gcg	cag	cag	tac	gtt	cca	ggg	ttg	gat	ggc	tgg	tca	cac	gcg	ctg	595	
Met	Ala	Gln	Gln	Tyr	Val	Pro	Gly	Leu	Asp	Gly	Trp	Ser	His	Ala	Leu		
150					155					160					165		
act	act	acc	tct	ggc	agc	ttt	gca	gag	gat	gca	gaa	aag	atc	ggc	gaa	643	
Thr	Thr	Thr	Ser	Gly	Ser	Phe	Ala	Glu	Asp	Ala	Glu	Lys	Ile	Gly	Glu		
				170					175					180			
gcc	acc	cgc	aat	gtt	cac	act	gct	ctt	gca	tgc	gcc	ttc	cct	act	cgg	691	
Ala	Thr	Arg	Asn	Val	His	Thr	Ala	Leu	Ala	Ser	Ala	Phe	Pro	Thr	Arg		
			185					190					195				
gta	gtt	ccc	gta	gaa	gca	ctc	gcc	gat	gcg	ctc	act	acc	cgc	ctt	aat	739	
Val	Val	Pro	Val	Glu	Ala	Leu	Ala	Asp	Ala	Leu	Thr	Thr	Arg	Leu	Asn		
		200					205					210					
gaa	cta	atc	tcc	caa	gca	ccc	gaa	atc	gcc	cgc	ttc	aaa	gaa	gca	gcc	787	
Glu	Leu	Ile	Ser	Gln	Ala	Pro	Glu	Ile	Ala	Arg	Phe	Lys	Glu	Ala	Ala		
	215					220					225						
atc	gac	ctc	tac	caa	tgc	ttg	gaa	ggc	gaa	gcc	cac	atc	caa	cgc	atc	835	
Ile	Asp	Leu	Tyr	Gln	Ser	Leu	Glu	Gly	Glu	Ala	His	Ile	Gln	Arg	Ile		
230					235					240					245		
cac	ggg	gac	ctc	cac	ttg	ggg	cag	ctc	atc	aaa	acc	ccc	gaa	cgc	tac	883	
His	Gly	Asp	Leu	His	Leu	Gly	Gln	Leu	Ile	Lys	Thr	Pro	Glu	Arg	Tyr		
				250					255					260			
atc	ctc	atc	gat	ttc	gaa	ggc	gaa	cct	gcc	cgc	cca	ctt	aat	caa	cga	931	
Ile	Leu	Ile	Asp	Phe	Glu	Gly	Glu	Pro	Ala	Arg	Pro	Leu	Asn	Gln	Arg		

265 270 275  
 cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979  
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser  
 280 285 290  
 atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac  
 1027  
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn  
 295 300 305  
 gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa  
 1075  
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln  
 310 315 320 325  
 gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc  
 1123  
 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala  
 330 335 340  
 tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg  
 1171  
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala  
 345 350 355  
 gtc gaa agg ctt cta gac tagttagtta ctctgcgtca aac  
 1212  
 Val Glu Arg Leu Leu Asp  
 360

&lt;210&gt; 1156

&lt;211&gt; 363

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1156

Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys  
 1 5 10 15  
 Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly  
 20 25 30  
 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu  
 35 40 45  
 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu  
 50 55 60  
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile  
 65 70 75 80  
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile  
 85 90 95  
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser  
 100 105 110  
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro  
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala  
 130 135 140  
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly  
 145 150 155 160  
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala  
 165 170 175  
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser  
 180 185 190  
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu  
 195 200 205  
 Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg  
 210 215 220  
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala  
 225 230 235 240  
 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys  
 245 250 255  
 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg  
 260 265 270  
 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala  
 275 280 285  
 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His  
 290 295 300  
 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly  
 305 310 315 320  
 Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala  
 325 330 335  
 Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys  
 340 345 350  
 Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp  
 355 360